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INHERITANCE OF SOYBEAN POD NUMBER TRAIT ON ACID SOIL

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ABSTRACT

Al-toxicity stressed soybean will show its tolerance response by changing pod number per plant. Hence, Al-toxicity tolerance of soybean can be predicted using that character. The objective of the research was to study inheritance of pod number trait of soybean on acid soil. Development of base population was carried out by crossing the genotypes of W3898-14-3 with MLGG 0583 and MLGG 0709. Thirteen populations resulting from soybean base population were grown on Ultisol with Al saturity of 32.84%. The design was randomized completely block design with three replications. Results showed that based on pod number per plant, soybean tolerance was polygenically controlled, where the gene action was additive and there was no allelic and non-allelic interaction genes. Narrow sense heritability was low, while broad sense heritability was classified as high. Based on high broad sense heritability and no genes interaction and polygenically gene control of pod number trait, selection can be carried out by choosing plants with low intensity of selection at medium generation to accelerate selection without losing many potential plants.

Keywords: Al-toxicity, gene action, heritability, pod number trait, soybean

INTRODUCTION

Selection criteria are the important component in developing a superior variety because it has main role in selecting the desired genotype. Developing Al-tolerant soybean variety requires a trait reflecting the tolerance. However, root trait is the best trait to be used as selection criterion for soybean tolerance to Al toxicity because Al toxicity symptoms were expressed especially on root growth inhibition, form changes, and root color changes (Rajaram *et al*., 1991). Besides, plant growth inhibition by Al toxicity usually can not be observed before symptoms on root occur. This statement is linear with Hanson's (1991) which stated that there was no shoot and root growth. In addition, type of roots also affects the soybean tolerance to Al toxicity (Bushamuka dan Zobel, 1998). Other Al toxicity symptoms were reported by Ritchey (1991) who stated that plant overcame decreasing on total root length growth, root length average and total root dry weight. However, these traits can not be used as selection criteria because the use of traits referring to the measurement or the use of root will be difficult in selecting genotypes tolerance to Al toxicity. The easiness of traits measurement or observation determined as selection criteria is very important because selection on segregating lines involves plant individual which is genetically different.

Physiological trait which is the base of response of a trait to stress environment can serve as selection criteria. However, the use of these selection criteria also depends on time and high cost in the implementation. Hence, selection criteria of Al toxicity tolerance should be directed on traits which can be measured easily and related to root traits and other physiological traits. Kuswantoro (2004) suggested that some traits of plant shoot can serve as attributes of tolerance to acid soil, where one of them is the number of pod per plant. Based on the correlation to physiological traits, number of pod is significantly correlated to root Mg content and ratio of root Al/(Ca+Mg) content. Pod number is also significantly correlated to root dry weight and seed yield.

Besides, heritability of pod number trait is classified as medium (Kuswantoro *et al*., 2006; Mursito, 2003), so selection using this trait will be relatively easier.

In breeding for acid soil tolerance, genetic study which is related to shoot traits (plant height, pods and branches number, and 100 seeds weight) is very important because they relate to selection criteria. Selection can not be conducted by observing roots because plant will be dead while seeds are needed for the next selection. Hence, some researchers observed shoot traits to be used as selection criteria (Bouton, 1996; Dall'Agnoll *et al*., 1996; Granados *et al*., 1993; Sledge *et al*., 2002). Caradus *et al*. (1991) reported diallel crossing to study genetics of *Trifolium repens* tolerance to Al toxicity based on shoot dry weight stated that the crossing of tolerance and susceptible genotypes described that Al tolerance trait was controlled by resesive gene. Further, narrow sense heritability was classified as high.

MATERIALS AND METHODS

Plant materials were two susceptible parents (MLGG 0583 and MLGG 0709) and one tolerant parent (W3898-14-3), and populations of F1, reciprocal-F1, F2, BC1 and BC2. Development of F1, reciprocal-F1, F2, BC1 and BC2 populations was conducted from March 2002 to January 2003 at Indonesian Legume and Tuber Crops Research Institute while the planting of three parents and five populations was conducted at Research Station of Vocational High School, Center of Tulang Bawang Tengah, Lampung, Indonesia. The soil was classified as Ultisols; Aldd was about 1.27-1.97 Cmol.kg^{-1}. In composite soil analysis, Aldd was 1.76 Cmol.kg^{-1}, pH H_2O 5.5, pH KCl 4.1 and Al saturity was 32.84%.

Crossing combinations:
Genetic population I:
MLGG 0583 x W3898-14-3
W3898-14-3 x MLGG 0583
(MLGG 0583 x W3898-14-3) x W3898-14-3
(MLGG 0583 x W3898-14-3) x MLGG 0583
Genetic population II:
MLGG 0709 x W3898-14-3
W3898-14-3 x MLGG 0709
(MLGG 0709 x W3898-14-3) x W3898-14-3
(MLGG 0709 x W3898-14-3) x MLGG 0709

The design was randomized completely block design with three replications. Two weeks before planting, soil was tilled and then hills were made. Spaces between the hills were made with drainage width and depth were 0.5 m and 0.2 m respectively. Plant spacing was 40 x 15 cm, and one seed was planted in one hole. Each genotype of parent, F1 and reciprocal-F1, was grown in 20 plants, while BC1 and BC2 were in 60 plants, and F2 was in 200 plants per block. Hence, there were 2340 plants in this research to be observed individually.

Estimation of three genetic parameters m (mean), d (sum of additive effect), and h (sum of dominance effect) was conducted in order to study the suitability of additive and dominance model. The suitability of the model was analyzed by comparing observation results to estimation value with X^2 test. This analysis was carried out according to Mather and Jinks (1971) and Singh dan Chaudary (1979) by using six equations to estimate three genetic parameters. If there was no non-allelic interaction, the three genetic parameters were equal to zero. If there was one or more parameter not equal to zero, it means there was a non-allelic interaction. If the analysis result showed non-allelic interaction genes, advanced test would be conducted by using six genetic parameters model.

Broad sense heritability estimated according to the following formula:

$$h^2_{b.s.} = \frac{\sigma^2_{F2} - (1/3)(\sigma^2_{F1} + \sigma^2_{P1} + \sigma^2_{P2})}{\sigma^2_{F2}}$$

Where:

$h^2_{b.s.}$ = broad sense heritability
σ^2_{F2} = variance of F_2 population
σ^2_{F1} = variance of F_1 population
σ^2_{P1} = variance of P_1 parent population
σ^2_{P2} = variance of P_2 parent population

Narrow sense heritability was estimated by using the following formula:

$$h^2_{n.s.} = \frac{2\sigma^2_{F2} - \sigma^2_{B1} - \sigma^2_{B2}}{\sigma^2_{F2}}$$

Where:

$h^2_{n.s.}$ = narrow sense heritability

σ^2_{F2} = variance of F_2 population

σ^2_{BC1} = variance of backcross population of P_1 parent

σ^2_{BC2} = variance of backcross population of P_2 parent

RESULTS AND DISCUSSION

Number of Controlling Genes

Distribution of F2 population genotypes based on the number of pods per plant for the crossing of MLGG 0583 x W3898-14-3 and MLGG 0709 x W3898-14-3 is presented on Fig. 1 and 2. Frequency distribution of F2 genotypes seems to have normal curve. The formed curve is not simetric but skew to the right side with the highest frequency at class of 30-40 pods per plant. Similar to the crossing of MLGG 0583 x W3898-14-3, on F2 population of MLGG 0709 x W3898-14-3 crossing, the curve is skew to the right side. Distribution with one peak indicates that pod number trait was controlled by polygenic genes, while non-simetric curve indicates the existence of dominance. However, of X^2 test and additive-dominance model, there was no dominance gene.

Polygenic genes controlling tolerance to Al toxicity causes frequency distribution to be continually curved (Fig. 1 and 2). Continual distribution on quantitative character can not be fitted to the discrete class (Rasmusson and Gengenbach, 1983). This continuity is caused by simultaneous segregation of many genes controlling the same character and non-genetic factor (Soemartono *et al.*, 1992).

Mathernal Effect

Result of mathernal effect test of MLGG 0583 X W3898-14-3 and MLGG 0709 X W3898-14-3 crossings were presented on Table 1. Of two crossing combination, there was no mathernal effect on the number of pods per plant. Sunarto (1985) also reported that there was no maternal effect, which means that the genes were in nucleus and not in the cytoplasmic. Average of pod number of F1 and r-F1 will be different if the maternal effect exists because cytoplasmic genes are in the female parent, so gene expression follows female parent.

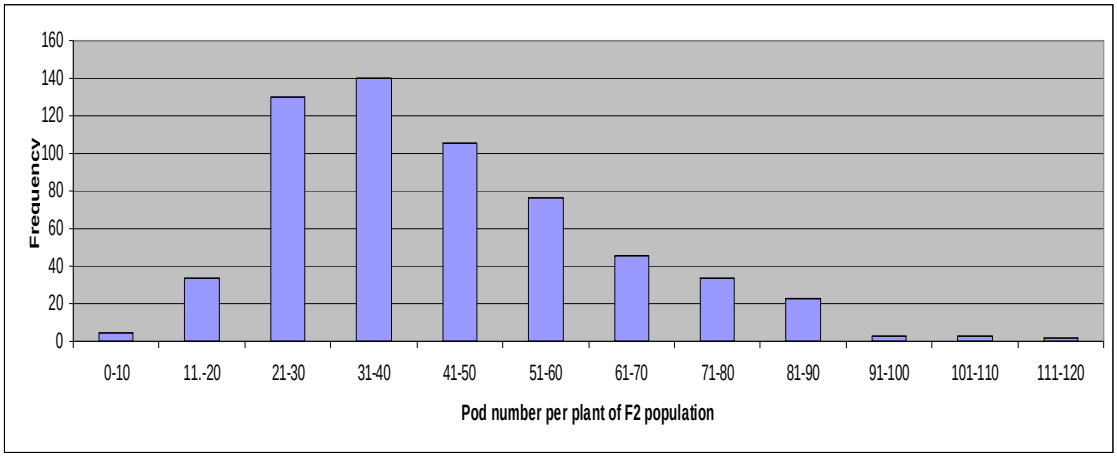

Figure 1. Genes frequency distribution of pods number per plant on F2 population of MLGG 0583 x W3898-14-3 crossing

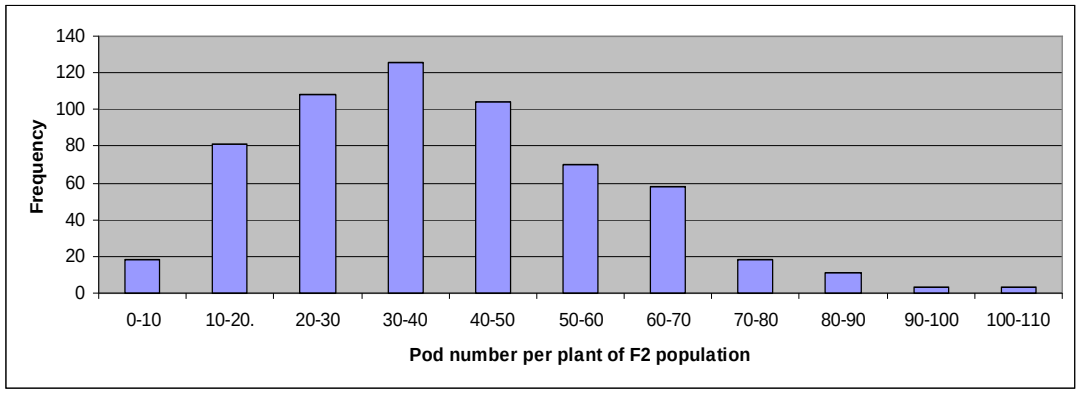

Figure 2. Genes frequency distribution of pod number per plant on F2 population of MLGG 0709 x W3898-14-3 crossing

Table 1. Maternal effect of MLGG 0583 X W3898-14-3 and MLGG 0709 X W3898-14-3 crossing

Population	Average of pod number	
	MLGG 0583 X W3898-14-3	MLGG 0709 X W3898-14-3
F1	42.13	39.51
r-F1	46.53	46.39
t hitung	1.24 ns	1.95 ns

Remarks: F1= F1 population, r-F1= reciprocal F1 population, ns = non significant at 5% level

Genes Action

Of joint scalling test, it is identified that soybean tolerance to acid soil was controlled by additive gene action and no maternal effect (Table 1-3). Gene additive effect controlling pod number trait of MLGG 0583 x W3898-14-3 crossing was significant, while dominance effect was not significant (Table 2). Additive-dominance model test shows that additive-dominance model fits the pod number trait (Table 3). Also, on MLGG 0709 x W3898-14-3 crossing, there is additive effect and no dominance effect (Table 2). However, the probability is lower, i.e. 0.10-0.25 (Table 3).

Additive effect is the effect caused by each allele without interaction with other genes (allelic or non-allelic interactions). The additive effect gives one unit value at phenotype resulting from additive gene without considering the allele contribution of the joined gametes. Suprapto and Kairudin (2007) also reported that pod number was controlled additively, where the additive contribution to genetic variance was 74.70%.The additive effect is important because it is the main cause of ressemblance between relatives, and it is the main determinant of genetic traits which can be observed from a population and determinant of population response to selection (Soemartono *et al*., 1992).

Effect of gene interaction will make a bias of assessment of an individual plant because at the next generation different result caused by segregations will be obtained. The different result occurs because the existence of gene is covered by other gene (allelic or non-allelic). On the other side, additive effect will improve from generation to the next generation. In this research, dominance effect was not significant, while fit test of additive-dominance was significant, which means that there was no non-allelic gene interaction. No epistatic effect in this research might occur due to many controlling genes (polygenic) so it might involve many loci. Epistatic will have high effect if it only involves two or three loci; if it involves four or more loci, the effect will be low and can be ignored (Soemartono *et al*., 1992).

Table 2. Additive-dominance effect of pod number characters of MLGG 0583 x W3898-14-3 and MLGG 0709 x W3898-14-3 crossings

Genetic parameters	MLGG 0583 x W3898-14-3		MLGG 0709 x W3898-14-3	
	Value	t calculated	Value	t calculated
m	43.932	23.268**	38.282	17.976**
[d]	-8.910	-4.912**	-11.045	4.982**
[h]	0.039	0.013	3.387	0.890

Remarks: **Significant at 1%, m=mean, [d]=aditive effect, [h]=dominance effect

Table 3. Fit test of additive-dominance model of pod number character of MLGG 0583 x W3898-14-3 and MLGG 0709 x W3898-14-3 crossings

Families population	X^2 calculated	
	MLGG 0583 x W3898-14-3	MLGG 0709 x W3898-14-3
P1	0.438	0.118
P2	1.029	0.184
F1	0.988	0.631
F2	0.006	0.054
B1	1.826	1.711
B2	0.431	1.581
X^2	4.717	4.280
P value	0.10-0.25	0.10-0.25

Remarks: P1= MLGG 0583 (parent 1), P2= W3898-14-3 (parent 2), F1= F1 of MLGG 0583 x W3898-14-3, F2= F2 of MLGG 0583 x W3898-14-3, B1=backcross of (MLGG 0583 x W3898-14-3) x MLGG 0583, B2=backcross of (MLGG 0583 x W3898-14-3) x W3898-14-3

Heritability

Broad and narrow sense heritabilities of MLGG 0583 X W3898-14-3 and MLGG 0709 X W3898-14-3 are presented in Table 4. Heritability has a role to determine if differences of observation within the individual are influenced by the differences in genetics constitution (Basuki, 1995). Heritability of a character can be defined as a proportion of genetic variance to units of genetic and environmental variance, or a proportion of genetic variance to phenotypic variance for a character. Falconer (1989) stated that the proportion defined degree of resemblance between relatives, but the main function of the heritability is the predictive role by expressions phenotypic value as breeding value. Heritability estimation serves in determination of expected selection gain and development of breeding strategy which is suitable by giving selection method and directions (Bari *et al*., 1974; and Pantalone *et al*., 1996).

Heritability estimation value of a character may differ depending on the calculation methods. The difference is affected by its character response to the environment growth. Value of $h^2_{b.s.}$ of pod number character in this research was classified as high according to Stansfield (1991) i.e. 0.53-0.57 (Table 4). At pod number character, Pinaria *et al*. (1995) reported heritability value of 0.55; while Adie (1992) reported heritability of 0.52-0.81. Suprapto and Kairudin (2007) also reported the height of $h^2_{b.s.}$ and $h^2_{n.s.}$ as 0.76 and 0.66 respectively, so with 5% selection intensity, genetic gain estimation will be obtained at 15.77%.

Pod number charater on both two crossings showed that value of $h^2_{n.s.}$ was medium. It means that environment and non-additive variances have important role. The medium value of $h^2_{n.s.}$ occurred because $h^2_{b.s.}$ values were not developed by high additive variance. Narrow sense heritability is determined by proportion of additive variance to phenotypic variance. Phenotypic variance is a result of additive variance, dominance variance, epistatic variance and environment variance. If

there are no dominance and epistatic variance, so $h^2_{n.s.} = h^2_{b.s.}$

Implication of Inheritance Genes to Soybean Breeding for Acid Soil Tolerance

Improvement of soybean tolerance to acid soil through improvement of pod number character will be effective because this character has no gene interaction (allelic or non-allelic). Gene additive role in this character is very useful in the selection, for this additive effect is the most important in the resemblance between an individual and its offsprings. The unexistence of gene interaction will ease the assessment in the selection. Besides, no gene interaction suggested that the assessment of selection efficiency and genetic gain can be conducted based on broad sense heritability (Viana, 2005). Hence, when there is no epistasis, additive gene effect is the suitable indicator for gene frequency changes following the selection (Wang *et al*., 2004). However, it requires a consideration because narrow sense heritability of pod number was medium, so selection will be more effective if selection is started at medium generation with low intensity and continued by bulk selection method.

The use of bulk selection will be able to improve or accumulate additive genes at advanced generation because the selection is conducted on advanced generation. Homozigosity of advanced generation is also higher so selected lines will not overcome many changes caused by gene segregation. Further, bulk selection method allow natural selection because the intolerant plants facing environment stress will inhibate the growth and die (Allard, 1960; Poespodarsono, 1988). It is important because on breeding for tolerance to acid soil, the tolerance related with the environment. Lines of crossings which are tolerant to soil acidity will show better performance and will be selected as superior lines which are tolerant to acid soil. Besides, bulk selection method will be more efficient because it can reduce the number of employees in handling segregation generation.

Table 4. Population variance and heritability of pod number of MLGG 0583 X W3898-14-3 and MLGG 0709 X W3898-14-3 crossings

Genetic parameters	Crossing combination	
	MLGG 0583 x W3898-14-3	MLGG 0709 x W3898-14-3
Variance:		
P1	172.24	143.33
P2	165.65	165.68
F1	173.30	147.41
F2	364.90	353.48
B1	264.89	268.82
B2	292.99	299.89
Heritability:		
h^2_{bs}	0.53	0.57
h^2_{ns}	0.47	0.39

Remarks: $h^2_{b.s.}$ = borad sense heritability, $h^2_{n.s.}$ = narrow sense heritability

CONCLUSIONS

Based on high broad sense heritability and no genes interaction, selection on pod number trait can be conducted on early generation. However, polygenically gene control of pod number trait suggested that selection should be conducted at advanced generation to avoid genes segregation at early generation. Hence, selection can be carried out by choosing plants with low intensity of selection at medium generation to accelerate selection without losing many potential plants.

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